

# SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDES ENCODING A NOVEL HUMAN PHOSPHATASE, BMY\_HPP13

<130> D0149 NP

<160> 40

<170> PatentIn version 3.2

<210> 1

<211> 989

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (26)..(763)

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Gln Thr Phe Gln Glu Leu Ile Gln Glu Ala Lys Pro Arg Ala Thr Trp
10          15          20          25

acg ctg aag ttg gat ggc aac ctt cag cta gac tgc ctg gct caa ggg      148
Thr Leu Lys Leu Asp Gly Asn Leu Gln Leu Asp Cys Leu Ala Gln Gly
          30          35          40

tgg aag caa tac caa cag aga gca ttt ggc tgg ttc cgg tgt tcc tcc      196
Trp Lys Gln Tyr Gln Gln Arg Ala Phe Gly Trp Phe Arg Cys Ser Ser
          45          50          55

tgc cag cga agt tgg gct tcc gcc caa gtg cag att ctg tgc cac acg      244
Cys Gln Arg Ser Trp Ala Ser Ala Gln Val Gln Ile Leu Cys His Thr
          60          65          70

tac tgg gag cac tgg aca tcc cag ggt cag gtg cgt atg agg ctc ttt      292
Tyr Trp Glu His Trp Thr Ser Gln Gly Gln Val Arg Met Arg Leu Phe
          75          80          85

ggc caa agg tgc cag aag tgc tcc tgg tcc caa tat gag atg cct gag      340
Gly Gln Arg Cys Gln Lys Cys Ser Trp Ser Gln Tyr Glu Met Pro Glu
90          95          100          105

ttc tcc tcg gat agc acc atg agg att ctg agc aac ctg gtg cag cat      388
Phe Ser Ser Asp Ser Thr Met Arg Ile Leu Ser Asn Leu Val Gln His
          110          115          120

ata ctg aag aaa tac tat gga aat ggc acg agg aag tct cca gaa atg      436
Ile Leu Lys Lys Tyr Tyr Gly Asn Gly Thr Arg Lys Ser Pro Glu Met

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|   |              |     |     |
|---|--------------|-----|-----|
| 125   | 130          | 135 |     |
| cca gta atc ctg gaa gtg tcc ctg gaa gga tcc cat gac aca gcc aat   |              |     | 484 |
| Pro Val Ile Leu Glu Val Ser Leu Glu Gly Ser His Asp Thr Ala Asn   |              |     |     |
| 140   | 145          | 150 |     |
| tgt gag gca tgc act ttg ggc atc tgt gga cag ggc tta aaa agc tgc   |              |     | 532 |
| Cys Glu Ala Cys Thr Leu Gly Ile Cys Gly Gln Gly Leu Lys Ser Cys   |              |     |     |
| 155   | 160          | 165 |     |
| atg aca aag ccg tcc aaa tcc cta ctc ccc cac cta aag act ggg aat   |              |     | 580 |
| Met Thr Lys Pro Ser Lys Ser Leu Leu Pro His Leu Lys Thr Gly Asn   |              |     |     |
| 170   | 175          | 180 | 185 |
| tcc tca cct gga att ggt gct gtg tac ctc gca aac caa gcc aag aac   |              |     | 628 |
| Ser Ser Pro Gly Ile Gly Ala Val Tyr Leu Ala Asn Gln Ala Lys Asn   |              |     |     |
| 190   | 195          | 200 |     |
| cag tca gct gag gca aaa gag gct aag ggg agt ggg tat gag aaa tta   |              |     | 676 |
| Gln Ser Ala Glu Ala Lys Glu Ala Lys Gly Ser Gly Tyr Glu Lys Leu   |              |     |     |
| 205   | 210          | 215 |     |
| ggg ccc agt cga gac cca gat cca ctg aac atc tgt gtc ttt att ttg   |              |     | 724 |
| Gly Pro Ser Arg Asp Pro Asp Pro Leu Asn Ile Cys Val Phe Ile Leu   |              |     |     |
| 220   | 225          | 230 |     |
| ctg ctt gta ttt att gta gtc aaa tgc ttt aca tca gaa tgatgaaaat    |              |     | 773 |
| Leu Leu Val Phe Ile Val Val Lys Cys Phe Thr Ser Glu               |              |     |     |
| 235   | 240          | 245 |     |
| aggcttgcca ctttctctta ttttaattcc atggtagtca atgaactggc tgccacttta |              |     | 833 |
| atataactga aaattcattt tgagaccaag caggatcaag tttgtagaat aaacactggg |              |     | 893 |
| ttcctagcca tcctctgaaa acagtatgaa acatgaccaa gtacataatg gatttagtaa |              |     | 953 |
| taaataattgt cgaattgcta aaaaaaaaaa aaaaag                          |              |     | 989 |
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| <213>   | Homo sapiens |     |     |
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| Met Val Val Asp Phe Trp Thr Trp Glu Gln Thr Phe Gln Glu Leu Ile   |              |     |     |
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| Gln Glu Ala Lys Pro Arg Ala Thr Trp Thr Leu Lys Leu Asp Gly Asn   |              |     |     |
| 20  | 25           | 30  |     |
| Leu Gln Leu Asp Cys Leu Ala Gln Gly Trp Lys Gln Tyr Gln Gln Arg   |              |     |     |
| 35  | 40           | 45  |     |

Ala Phe Gly Trp Phe Arg Cys Ser Ser Cys Gln Arg Ser Trp Ala Ser  
50 55 60

Ala Gln Val Gln Ile Leu Cys His Thr Tyr Trp Glu His Trp Thr Ser  
65 70 75 80

Gln Gly Gln Val Arg Met Arg Leu Phe Gly Gln Arg Cys Gln Lys Cys  
85 90 95

Ser Trp Ser Gln Tyr Glu Met Pro Glu Phe Ser Ser Asp Ser Thr Met  
100 105 110

Arg Ile Leu Ser Asn Leu Val Gln His Ile Leu Lys Lys Tyr Tyr Gly  
115 120 125

Asn Gly Thr Arg Lys Ser Pro Glu Met Pro Val Ile Leu Glu Val Ser  
130 135 140

Leu Glu Gly Ser His Asp Thr Ala Asn Cys Glu Ala Cys Thr Leu Gly  
145 150 155 160

Ile Cys Gly Gln Gly Leu Lys Ser Cys Met Thr Lys Pro Ser Lys Ser  
165 170 175

Leu Leu Pro His Leu Lys Thr Gly Asn Ser Ser Pro Gly Ile Gly Ala  
180 185 190

Val Tyr Leu Ala Asn Gln Ala Lys Asn Gln Ser Ala Glu Ala Lys Glu  
195 200 205

Ala Lys Gly Ser Gly Tyr Glu Lys Leu Gly Pro Ser Arg Asp Pro Asp  
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Pro Leu Asn Ile Cys Val Phe Ile Leu Leu Leu Val Phe Ile Val Val  
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Lys Cys Phe Thr Ser Glu  
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| Met Arg Val Ile Glu Gly Lys Gly Phe Ala Gln Gly Leu Pro Asp Val |     |
| 1 5 10 15   |     |
| aac tgg atc ttc aac cca ggt tcc ggt gtt cct cct gcc agc gaa gtt | 96  |
| Asn Trp Ile Phe Asn Pro Gly Ser Gly Val Pro Pro Ala Ser Glu Val |     |
| 20 25 30  |     |
| ggg ctt ccg ccc aag tgc aga ttc tgt gcc aca cgt act ggg agc act | 144 |
| Gly Leu Pro Pro Lys Cys Arg Phe Cys Ala Thr Arg Thr Gly Ser Thr |     |
| 35 40 45  |     |
| gga cat ccc agg gtc agg tgc cag aag tgc tcc tgg tcc caa tat gag | 192 |
| Gly His Pro Arg Val Arg Cys Gln Lys Cys Ser Trp Ser Gln Tyr Glu |     |
| 50 55 60  |     |
| atg cct gag ttc tcc tcg gat agc acc atg agg att ctg agc aac ctg | 240 |
| Met Pro Glu Phe Ser Ser Asp Ser Thr Met Arg Ile Leu Ser Asn Leu |     |
| 65 70 75 80   |     |
| gtg cag cat ata ctg aag aaa tac tat gga aat ggc acg agg aag tct | 288 |
| Val Gln His Ile Leu Lys Lys Tyr Tyr Gly Asn Gly Thr Arg Lys Ser |     |
| 85 90 95  |     |
| cca gaa atg cca gta atc ctg gaa gtg tcc ctg gaa gga tcc cat gac | 336 |
| Pro Glu Met Pro Val Ile Leu Glu Val Ser Leu Glu Gly Ser His Asp |     |
| 100 105 110   |     |
| aca gcc aat tgt gag gca tgc act ttg ggc atc tgt gga cag ggc tta | 384 |
| Thr Ala Asn Cys Glu Ala Cys Thr Leu Gly Ile Cys Gly Gln Gly Leu |     |
| 115 120 125   |     |
| aaa agc tgc atg aca aag ccg tcc aaa tcc cta ctc ccc cac cta aag | 432 |
| Lys Ser Cys Met Thr Lys Pro Ser Lys Ser Leu Leu Pro His Leu Lys |     |
| 130 135 140   |     |
| act ggg aat tcc tca cct gga att ggt gct gtg tac ctc gca aac caa | 480 |
| Thr Gly Asn Ser Ser Pro Gly Ile Gly Ala Val Tyr Leu Ala Asn Gln |     |
| 145 150 155 160   |     |
| gcc aag aac cag tca gct gag gca aaa gag gct aag ggg agt ggg tat | 528 |
| Ala Lys Asn Gln Ser Ala Glu Ala Lys Glu Ala Lys Gly Ser Gly Tyr |     |
| 165 170 175   |     |
| gag aaa tta ggg ccc agt cga gac cca gat cca ctg aac atc tgt gtc | 576 |
| Glu Lys Leu Gly Pro Ser Arg Asp Pro Asp Pro Leu Asn Ile Cys Val |     |
| 180 185 190   |     |
| ttt att ttg ctg ctt gta ttt att gta gtc aaa tgc ttt aca tca gaa | 624 |
| Phe Ile Leu Leu Leu Val Phe Ile Val Val Lys Cys Phe Thr Ser Glu |     |

195

200

205

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Met Arg Val Ile Glu Gly Lys Gly Phe Ala Gln Gly Leu Pro Asp Val  
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Asn Trp Ile Phe Asn Pro Gly Ser Gly Val Pro Pro Ala Ser Glu Val  
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Gly Leu Pro Pro Lys Cys Arg Phe Cys Ala Thr Arg Thr Gly Ser Thr  
 35 40 45

Gly His Pro Arg Val Arg Cys Gln Lys Cys Ser Trp Ser Gln Tyr Glu  
 50 55 60

Met Pro Glu Phe Ser Ser Asp Ser Thr Met Arg Ile Leu Ser Asn Leu  
 65 70 75 80

Val Gln His Ile Leu Lys Lys Tyr Tyr Gly Asn Gly Thr Arg Lys Ser  
 85 90 95

Pro Glu Met Pro Val Ile Leu Glu Val Ser Leu Glu Gly Ser His Asp  
 100 105 110

Thr Ala Asn Cys Glu Ala Cys Thr Leu Gly Ile Cys Gly Gln Gly Leu  
 115 120 125

Lys Ser Cys Met Thr Lys Pro Ser Lys Ser Leu Leu Pro His Leu Lys  
 130 135 140

Thr Gly Asn Ser Ser Pro Gly Ile Gly Ala Val Tyr Leu Ala Asn Gln  
 145 150 155 160

Ala Lys Asn Gln Ser Ala Glu Ala Lys Glu Ala Lys Gly Ser Gly Tyr  
 165 170 175

Glu Lys Leu Gly Pro Ser Arg Asp Pro Asp Pro Leu Asn Ile Cys Val  
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Phe Ile Leu Leu Leu Val Phe Ile Val Val Lys Cys Phe Thr Ser Glu  
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Asp Tyr Ile Asn Ala Ser Asn  
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<400> 8

Asp Asn Tyr Ile Asn Ala Ser Asn  
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Ala Gly Val Cys Gly Gly Ala Gln Arg Pro Gly His Leu Pro Gly Leu  
20 25 30

Leu Leu Gly Ser His Gly Leu Leu Gly Ser Pro Val Arg Ala Ala Ala  
35 40 45

Ser Ser Pro Val Thr Thr Leu Thr Gln Thr Met His Asp Leu Ala Gly  
 50 55 60

Leu Gly Ser Arg Ser Arg Leu Thr His Leu Ser Leu Ser Arg Arg Ala  
 65 70 75 80

Ser Glu Ser Ser Leu Ser Ser Glu Ser Ser Glu Ser Ser Asp Ala Gly  
 85 90 95

Leu Cys Met Asp Ser Pro Ser Pro Met Asp Pro His Met Ala Glu Gln  
 100 105 110

Thr Phe Glu Gln Ala Ile Gln Ala Ala Ser Arg Ile Ile Arg Asn Glu  
 115 120 125

Gln Phe Ala Ile Arg Arg Phe Gln Ser Met Pro Val Arg Leu Leu Gly  
 130 135 140

His Ser Pro Val Leu Arg Asn Ile Thr Asn Ser Gln Ala Pro Asp Gly  
 145 150 155 160

Arg Arg Lys Ser Glu Ala Gly Ser Gly Ala Ala Ser Ser Ser Gly Glu  
 165 170 175

Asp Lys Glu Asn Asp Gly Phe Val Phe Lys Met Pro Trp Lys Pro Thr  
 180 185 190

His Pro Ser Ser Thr His Ala Leu Ala Glu Trp Ala Ser Arg Arg Glu  
 195 200 205

Ala Phe Ala Gln Arg Pro Ser Ser Ala Pro Asp Leu Met Cys Leu Ser  
 210 215 220

Pro Asp Arg Lys Met Glu Val Glu Glu Leu Ser Pro Leu Ala Leu Gly  
 225 230 235 240

Arg Phe Ser Leu Thr Pro Ala Glu Gly Asp Thr Glu Glu Asp Asp Gly  
 245 250 255

Phe Val Asp Ile Leu Glu Ser Asp Leu Lys Asp Asp Asp Ala Val Pro  
 260 265 270

Pro Gly Met Glu Ser Leu Ile Ser Ala Pro Leu Val Lys Thr Leu Glu



|   |     |     |     |     |
|---|-----|-----|-----|-----|
| 275   |     | 280 |     | 285 |
| Lys Glu Glu Glu Lys Asp Leu Val Met Tyr Ser Lys Cys Gln Arg Leu | 290 | 295 | 300 |     |
| Phe Arg Ser Pro Ser Met Pro Cys Ser Val Ile Arg Pro Ile Leu Lys | 305 | 310 | 315 | 320 |
| Arg Leu Glu Arg Pro Gln Asp Arg Asp Thr Pro Val Gln Asn Lys Arg | 325 | 330 | 335 |     |
| Arg Arg Ser Val Thr Pro Pro Glu Glu Gln Gln Glu Ala Glu Glu Pro | 340 | 345 | 350 |     |
| Lys Ala Arg Val Leu Arg Ser Lys Ser Leu Cys His Asp Glu Ile Glu | 355 | 360 | 365 |     |
| Asn Leu Leu Asp Ser Asp His Arg Glu Leu Ile Gly Asp Tyr Ser Lys | 370 | 375 | 380 |     |
| Ala Phe Leu Leu Gln Thr Val Asp Gly Lys His Gln Asp Leu Lys Tyr | 385 | 390 | 395 | 400 |
| Ile Ser Pro Glu Thr Met Val Ala Leu Leu Thr Gly Lys Phe Ser Asn | 405 | 410 | 415 |     |
| Ile Val Asp Lys Phe Val Ile Val Asp Cys Arg Tyr Pro Tyr Glu Tyr | 420 | 425 | 430 |     |
| Glu Gly Gly His Ile Lys Thr Ala Val Asn Leu Pro Leu Glu Arg Asp | 435 | 440 | 445 |     |
| Ala Glu Ser Phe Leu Leu Lys Ser Pro Ile Ala Pro Cys Ser Leu Asp | 450 | 455 | 460 |     |
| Lys Arg Val Ile Leu Ile Phe His Cys Glu Phe Ser Ser Glu Arg Gly | 465 | 470 | 475 | 480 |
| Pro Arg Met Cys Arg Phe Ile Arg Glu Arg Asp Arg Ala Val Asn Asp | 485 | 490 | 495 |     |
| Tyr Pro Ser Leu Tyr Tyr Pro Glu Met Tyr Ile Leu Lys Gly Gly Tyr | 500 | 505 | 510 |     |

Lys Glu Phe Phe Pro Gln His Pro Asn Phe Cys Glu Pro Gln Asp Tyr  
515 520 525

Arg Pro Met Asn His Glu Ala Phe Lys Asp Glu Leu Lys Thr Phe Arg  
530 535 540

Leu Lys Thr Arg Ser Trp Ala Gly Glu Arg Ser Arg Arg Glu Leu Cys  
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Ser Arg Leu Gln Asp Gln  
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cgacgacggt cggtcgagat ggtatgatgc gtaataaact atccccaag attcgagggt 180  
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| Met | Lys | Ser | Arg | Arg | Trp | Phe | His | Pro | Asn | Ile | Thr | Gly | Val | Glu | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Glu | Asn | Leu | Leu | Leu | Thr | Arg | Gly | Val | Asp | Gly | Ser | Phe | Leu | Ala | Arg |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Pro | Ser | Lys | Ser | Asn | Pro | Gly | Asp | Leu | Thr | Leu | Ser | Val | Arg | Arg | Asn |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Gly | Ala | Val | Thr | His | Ile | Lys | Ile | Gln | Asn | Thr | Gly | Asp | Tyr | Tyr | Asp |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Leu | Tyr | Gly | Gly | Glu | Lys | Phe | Ala | Thr | Leu | Ala | Glu | Leu | Val | Gln | Tyr |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Tyr | Met | Glu | His | His | Gly | Gln | Leu | Lys | Glu | Lys | Asn | Gly | Asp | Val | Ile |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Glu | Leu | Lys | Tyr | Pro | Leu | Asn | Cys | Ala | Asp | Pro | Thr | Ser | Glu | Arg | Trp |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Phe | His | Gly | His | Leu | Ser | Gly | Lys | Glu | Ala | Glu | Lys | Leu | Leu | Thr | Glu |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Lys | Gly | Lys | His | Gly | Ser | Phe | Leu | Val | Arg | Glu | Ser | Gln | Ser | His | Pro |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Gly | Asp | Phe | Val | Leu | Ser | Val | Arg | Thr | Gly | Asp | Asp | Lys | Gly | Glu | Ser |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Asn | Asp | Gly | Lys | Ser | Lys | Val | Thr | His | Val | Met | Ile | Arg | Cys | Gln | Glu |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Leu | Lys | Tyr | Asp | Val | Gly | Gly | Gly | Glu | Arg | Phe | Asp | Ser | Leu | Thr | Asp |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |

Leu Val Glu His Tyr Lys Lys Asn Pro Met Val Glu Thr Leu Gly Thr  
 195 200 205

Val Leu Gln Leu Lys Gln Pro Leu Asn Thr Thr Arg Ile Asn Ala Ala  
 210 215 220

Glu Ile Glu Ser Arg Val Arg Glu Leu Ser Lys Leu Ala Glu Thr Thr  
 225 230 235 240

Asp Lys Val Lys Gln Gly Phe Trp Glu Glu Phe Glu Thr Leu Gln Gln  
 245 250 255

Gln Glu Cys Lys Leu Leu Tyr Ser Arg Lys Glu Gly Gln Arg Gln Glu  
 260 265 270

Asn Lys Asn Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Thr  
 275 280 285

Arg Val Val Leu His Asp Gly Asp Pro Asn Glu Pro Val Ser Asp Tyr  
 290 295 300

Ile Asn Ala Asn Ile Ile Met Pro Glu Phe Glu Thr Lys Cys Asn Asn  
 305 310 315 320

Ser Lys Pro Lys Lys Ser Tyr Ile Ala Thr Gln Gly Cys Leu Gln Asn  
 325 330 335

Thr Val Asn Asp Phe Trp Arg Met Val Phe Gln Glu Asn Ser Arg Val  
 340 345 350

Ile Val Met Thr Thr Lys Glu Val Glu Arg Gly Lys Ser Lys Cys Val  
 355 360 365

Lys Tyr Trp Pro Asp Glu Tyr Ala Leu Lys Glu Tyr Gly Val Met Arg  
 370 375 380

Val Arg Asn Val Lys Glu Ser Ala Ala His Asp Tyr Thr Leu Arg Glu  
 385 390 395 400

Leu Lys Leu Ser Lys Val Gly Gln Gly Asn Thr Glu Arg Thr Val Trp  
 405 410 415

Gln Tyr His Phe Arg Thr Trp Pro Asp His Gly Val Pro Ser Asp Pro  
420 425 430

Gly Gly Val Leu Asp Phe Leu Glu Glu Val His His Lys Gln Glu Ser  
435 440 445

Ile Met Asp Ala Gly Pro Val Val Val His Cys Ser Ala Gly Ile Gly  
450 455 460

Arg Thr Gly Thr Phe Ile Val Ile Asp Ile Leu Ile Asp Ile Ile Arg  
465 470 475 480

Glu Lys Gly Val Asp Cys Asp Ile Asp Val Pro Lys Thr Ile Gln Met  
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Val Arg Ser Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Arg  
500 505 510

Ser Ile Tyr Met Ala Val Gln His Tyr Ile Glu Thr Leu  
515 520 525

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Lys Lys Tyr Tyr Gly Asn Gly Thr Arg Lys Ser Pro Glu Met  
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Phe Ser Ser Asp Ser Thr Met Arg Ile Leu Ser Asn Leu  
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Trp Thr Trp Glu Gln Thr Phe Gln Glu Leu Ile Gln Glu Ala  
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Gln Ile Leu Cys His Thr Tyr Trp Glu His Trp Thr Ser Gln  
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Gln Lys Cys Ser Trp Ser Gln Tyr Glu Met Pro Glu Phe Ser  
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Lys Glu Ala Lys Gly Ser Gly Tyr Glu Lys Leu Gly Pro Ser  
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 <212> PRT  
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<400> 26

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 1 5 10 15

<210> 27  
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<400> 27

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<210> 28  
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 tccccttagc ctcttttgcc 80

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 <213> Bacteriophage T7

<400> 29  
 taatacgact cactataggg 20

<210> 30  
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 <400> 30  
 atttaggtga cactatag 18  
  
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 tcccaatatg agatgcctga 20  
  
 <210> 32  
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 <213> bacteriophage T7  
  
 <400> 33  
 Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5  
  
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 <211> 733  
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 aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga 120  
 tctcccgga tcttgaggtc acatgcgtgg tggaggacgt aagccacgaa gacctgagg 180  
 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240  
 aggagcagta caacagcagc taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300  
 ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg 360  
 agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420  
 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct 480



|   |     |
|---|-----|
| atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga | 540 |
| ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctacagcaag ctcaccgtgg | 600 |
| acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc | 660 |
| acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc | 720 |
| gactctagag gat  | 733 |

<210> 35  
 <211> 38  
 <212> DNA  
 <213> Homo sapiens

|   |    |
|---|----|
| <400> 35                                  |    |
| gcagcagcgg ccgcgaggca aaaccccggg ccacatgg | 38 |

<210> 36  
 <211> 36  
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|   |    |
|---|----|
| <400> 36                                |    |
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<210> 37  
 <211> 39  
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|  |    |
|--|----|
| <400> 37                                   |    |
| gcagcagcgg ccgcatgggt gtagatttct ggacttggg | 39 |

<210> 38  
 <211> 37  
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|  |    |
|--|----|
| <400> 38                                 |    |
| gcagcagtcg accccactcc ccttagcctc ttttgcc | 37 |

<210> 39  
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<400> 39

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Leu | Asn | Ile | Cys | Val | Phe | Ile | Leu | Leu | Leu | Val | Phe | Ile | Val | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

Lys Cys Phe

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Ala Ile Tyr Gln Asp Ile Arg His Glu Ala Ser Asp Phe Pro Cys Arg  
20 25 30

Val Ala Lys Leu Pro Lys Asn Lys Asn Arg Asn Arg Tyr Arg Asp Val  
35 40 45

Ser Pro Phe Asp His Ser Arg Ile Lys Leu His Gln Glu Asp Asn Asp  
50 55 60

Tyr Ile Asn Ala Ser Leu Ile Lys Met Glu Glu Ala Gln Arg Ser Tyr  
65 70 75 80

Ile Leu Thr Gln Gly Pro Leu Pro Asn Thr Cys Gly His Phe Trp Glu  
85 90 95

Met Val Trp Glu Gln Lys Ser Arg Gly Val Val Met Leu Asn Arg Val  
100 105 110

Met Glu Lys Gly Ser Leu Lys Cys Ala Gln Tyr Trp Pro Gln Lys Glu  
115 120 125

Glu Lys Glu Met Ile Phe Glu Asp Thr Asn Leu Lys Leu Thr Leu Ile  
130 135 140

Ser Glu Asp Ile Lys Ser Tyr Tyr Thr Val Arg Gln Leu Glu Leu Glu  
145 150 155 160

Asn Leu Thr Thr Gln Glu Thr Arg Glu Ile Leu His Phe His Tyr Thr  
165 170 175

Thr Trp Pro Asp Phe Gly Val Pro Glu Ser Pro Ala Ser Phe Leu Asn  
180 185 190

Phe Leu Phe Lys Val Arg Glu Ser Gly Ser Leu Ser Pro Glu His Gly  
195 200 205

Pro Val Val Val His Ser Ser Ala Gly Ile Gly Arg Ser Gly Thr Phe  
210 215 220

Cys Leu Ala Asp Thr Cys Leu Leu Leu Met Asp Lys Arg Lys Asp Pro  
225 230 235 240

Ser Ser Val Asp Ile Lys Lys Val Leu Leu Glu Met Arg Lys Phe Arg  
245 250 255

Met Gly Leu Ile Gln Thr Ala Asp Gln Leu Arg Phe Ser Tyr Leu Ala  
260 265 270

Val Ile Glu Gly Ala Lys Phe Ile Met Gly Asp Ser Ser Val Gln Asp  
275 280 285

Gln Trp Lys Glu Leu Ser His Glu Asp  
290 295